



01 13 06 SeqListg CEN0250NP.txt

<110> Giles-Komar, Jill; David Shealy; David Knight; Bernie Scallon; George Heavner  
<120> ANTI-TNF ANTIBODIES, COMPOSITIONS, METHODS AND USES  
<130> CEN0250 NP  
<140> US 09/920,137  
<141> 2001-08-01  
<150> 60/223,360  
<151> 2000-08-07  
<150> 60/236,826  
<151> 2000-09-29  
<160> 35  
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<210> 1  
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<223> xaa at position 1 is selected from Ile, Phe or Val.  
  
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<223> xaa at position 2 is selected from Ile or Met.  
  
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<222> (3)..(3)  
<223> Xaa at position 3 is selected from Ser or Leu.

<220>  
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<222> (4)..(4)  
<223> Xaa at position 4 is selected from Tyr or Phe.

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<222> (10)..(10)  
<223> Xaa at position 10 is selected from Lys or Tyr.

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<222> (11)..(11)  
<223> Xaa at position 11 is selected from Ser or Tyr.

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<222> (17)..(17)  
<223> Xaa at position 17 is selected from Asp or Gly.

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1 Xaa Xaa Xaa Xaa Asp Gly Ser Asn Lys Xaa Xaa Ala Asp Ser Val Lys Xaa  
5 10 15

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<223> Heavy Chain complementarity determining region 3 (CDR3).

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<223> Xaa at position 4 is selected from Ile or Val.

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<222> (5)..(5)  
<223> Xaa at position 5 is selected from Ser, Ala or Gly.

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<222> (9)..(9)  
<223> Xaa at position 9 is selected from Asn or Tyr.

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1 Asp Arg Gly Xaa Xaa Ala Gly Gly Xaa Tyr Tyr Tyr Tyr Gly Met Asp Val  
5 10 15

<210> 4  
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<213> Homo sapiens

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<212> PRT  
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Gln Val Gln Leu Val Glu Ser Gly Gly Val Val Gln Pro Gly Arg  
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ile Phe Ser Ser Tyr  
20 25 30

Ala Met His Trp Val Arg Gln Ala Pro Gly Asn Gly Leu Glu Trp Val  
35 40 45

Ala Phe Met Ser Tyr Asp Gly Ser Asn Lys Lys Tyr Ala Asp Ser Val  
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55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr  
65 70 75 80  
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
85 90 95  
Ala Arg Asp Arg Gly Ile Ala Ala Gly Gly Asn Tyr Tyr Tyr Gly  
100 105 110  
Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser  
115 120 125

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Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly  
1 5 10 15  
Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Tyr Ser Tyr  
20 25 30  
Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile  
35 40 45  
Tyr Asp Ala Ser Asn Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly  
50 55 60  
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro  
65 70 75 80  
Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Arg Ser Asn Trp Pro Pro  
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Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys  
100 105

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Ala Asn Ala Leu Leu Ala Asn Gly Val Glu Leu Arg Asp Asn Gln Leu

val val Pro Ser Glu Gly Leu Tyr Leu Ile Tyr Ser Gln Val Leu Phe  
 50 55 60

Lys Gly Gln Gly Cys Pro Ser Thr His Val Leu Leu Thr His Thr Ile  
 65 70 75 80

Ser Arg Ile Ala val Ser Tyr Gln Thr Lys Val Asn Leu Leu Ser Ala  
 85 90 95

Ile Lys Ser Pro Cys Gln Arg Glu Thr Pro Glu Gly Ala Glu Ala Lys  
 100 105 110

Pro Trp Tyr Glu Pro Ile Tyr Leu Gly Gly Val Phe Gln Leu Glu Lys  
 115 120 125

Gly Asp Arg Leu Ser Ala Glu Ile Asn Arg Pro Asp Tyr Leu Asp Phe  
 130 135 140

Ala Glu Ser Gly Gln Val Tyr Phe Gly Ile Ile Ala Leu  
 145 150 155

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<213> Homo sapiens

<400> 11

cacctgcact cggtgctt 18

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<211> 30

<212> DNA

<213> Homo sapiens

<400> 12

cactgttttg agtgtgtacg ggcttaagtt 30

<210> 13

<211> 18

<212> DNA

<213> Homo sapiens

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gccgcacgtg tggaaagg 18

<210> 14

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<212> DNA  
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Met Asp Met Arg Val  
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<223> Signal sequence for heavy chain variable region sequences as presented in original  
  
Figure 4  
  
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1 5 10 15  
  
Val Gln Cys  
  
<210> 33  
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&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; MISC\_FEATURE

&lt;222&gt; (1)..(20)

&lt;223&gt; Signal sequence for light chain variable region sequences as presented in original

Figure 5

&lt;400&gt; 33

Met	Glu	Ala	Pro	Ala	Gln	Leu	Leu	Phe	Leu	Leu	Leu	Leu	Trp	Leu	Pro
1				5					10					15	
Asp	Thr	Thr	Gly												
			20												

&lt;210&gt; 34

&lt;211&gt; 428

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(421)

&lt;223&gt; heavy chain variable region DNA sequences as presented in original Figure 2A-2B

&lt;400&gt; 34

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tgtgcagcct ctggttcacc ttcagtagct atgctatgca ctgggtccgc caggctccgg 180
caagggctg gagtgggtgg cagttatatc atatgatgga aaataaaatac tacgcagact 240
ccgtgaaggg ccgattcacc atctagagac aattccaaga acacgctgta tctgcaaatg 300
aacagccaga gctgaggaca cggctgtgta ttactgtgcg agagatcgag gtatatcagc 360
aggtggaata ctactactac tacggtatgg acgtctgggg gcaagggacc acggtcaccg 420
tctcctca                                         428

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&lt;210&gt; 35

&lt;211&gt; 387

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(387)

&lt;223&gt; light chain variable region DNA sequences as presented in original Figure 3

&lt;400&gt; 35

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ctctcctgca gggccagtca gagtggtagc agctacttag cctggtagca acagaaacct 180
ggccaggctc ccaggctcct catctatgat gcatccaaca gggccactgg catcccagcc 240
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cctgggacca aagtggatataaaac 387

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